

Fig. 1

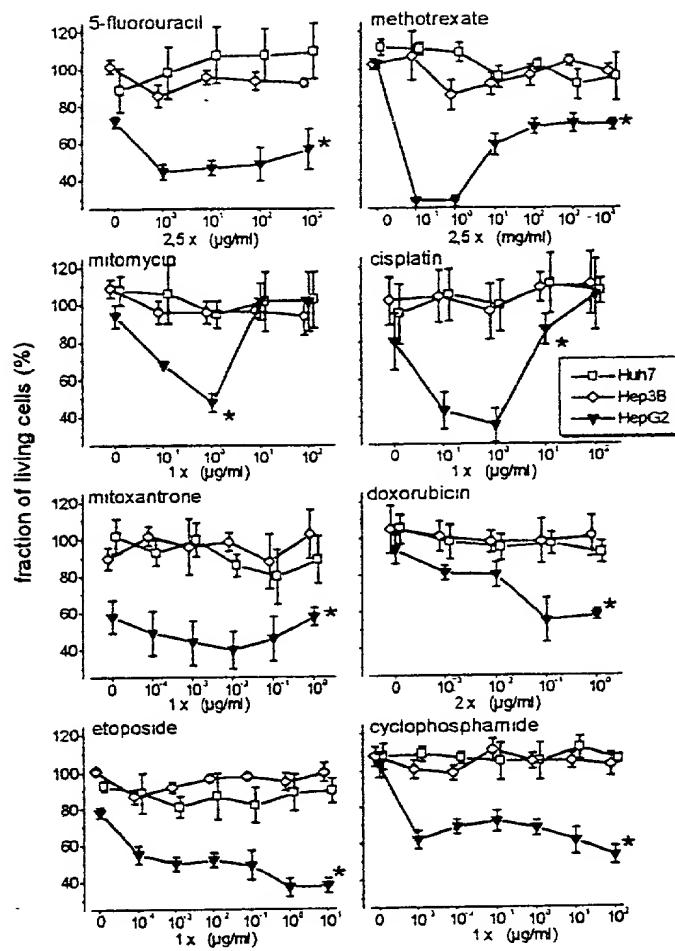


Fig. 2

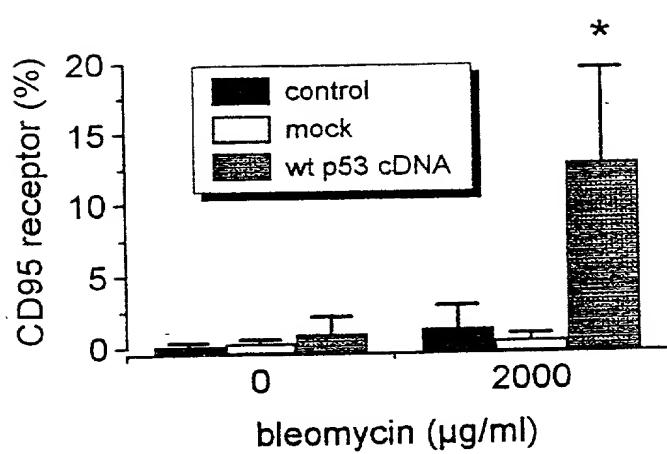


Fig. 3

620 GATCCCGCTGGGCAGGCGGG 640 GCAGCTCCGGCGCTCCCTGG 660 AGACCACTGCCTCCACGTT
Sau3A1

800 820 840
GCCAAAGGTCCGCTCCGGCG CGGGTGGGTGAGTGCGCGCC GCCCCCGCGGGGGCGGGGGAGA

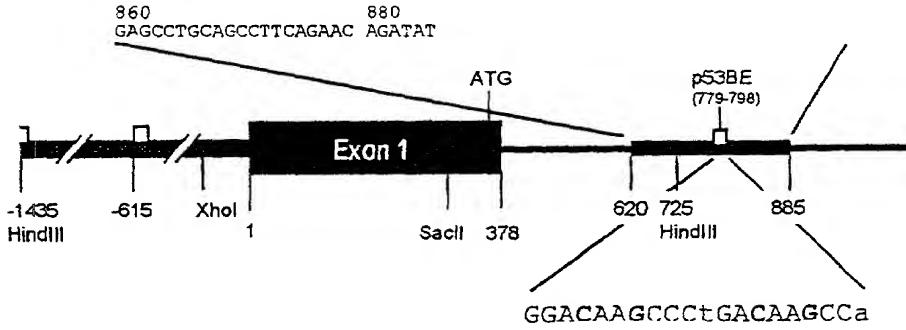


Fig. 4

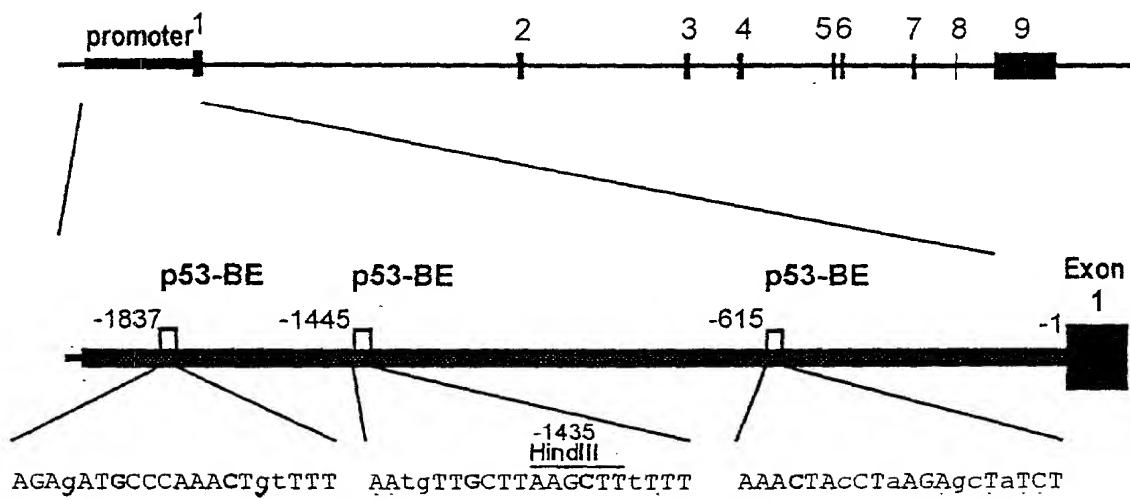


Fig. 5

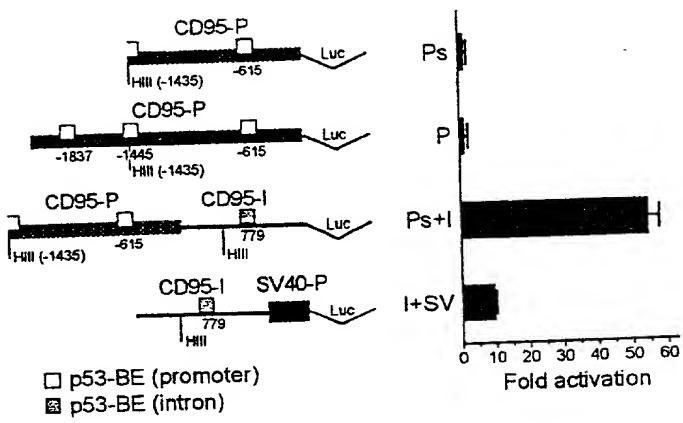


Fig. 6

GATCCCGCTGGCAGGCAGGGCAGCTCCGGCGCTCCTCGGAGACCACGTGCGCTCCACGTT
1 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 60
CTAGGGCGACCCGTCCGCCCGTCGAGGCCGAGGAGCCTCTGGTACGCGAGGTGCAA

GAGGTGGGCGTGGGGGGCGGACAGGAATTGAAGCGGAAGTCTGGGAAGCTTAGGGTCGC
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120
CTCCACCCGCACCCCCCGCTGTCCCTAACCGCCTCAGACCCCTCGAAATCCCAGCG

<---- 4.P53-BE ---->
(intron)
TGGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAA
121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 180
ACCTCCCCCTGGGGCAACCTCTCCTCGCCTTGAGGACCTGTTGGGACTGTTGGTT

GCCAAAGGTCCGCTCCGGCGCGGGTGGGTGAGTGCAGCGCCGCCCGCGGGGGCGGGGAGA
181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 240
CGGTTCCAGGCGAGGCCGCGCCACCCACTCACGCGGGCGGGCGCCCCCGCCCTCT

GAGCCTACAGCCTTCAGAACACATATTGCTCATTTCTGGCAGTTCTCAGACGTAGGAAA
241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 300
CTCGGATGTCGGAAGTCTTGTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTT

TAAGTCAGCACCGAACGAGTGGTTAACCGGGCTCGGAAGAACGGCACCTTCTTT
301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 360
ATTCAAGTCGTGGCTTCGTACCCAATTGGCCTCCGAGCCTTCTGGCGTGGAAAAGAAA

CTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTTGTACCGTTTTATT
361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 420
GAGCTTTCAATATACCCCCGACTTACTCGAACGACCTCCGAACAAATGGCAAAAATAA

GTCACACAGAAAAGGAAACTGCCCTGTCTCCCTCCGGAAATTCTCTCTTTAACGACTGTA
421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 480
CAGTGTGTCTTCCCTTGACGAAACAGAGGGAGGCCCTAACAGAGAGAAAATTCTGACAT

AGTCGCTGCCCTGAGTGGTTCTTTGTTCTGCCCTCTCTCTCTCTCTCTCTCT
481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 540
TCAGCGACGGACTACCAAAAGTAAAACAAAACAAAAGACGGGAAGAGAAAAGAAGAAAAC

CCCTTCTTAGCTGCACTCCCCTGGTATTCCTGCTGGTCTCTGCTGGGGTTGGTGG
541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 600
GGGAAAAGAACGAACTGAGGGTACCAACTAAAGACGAACCGAGAGGACGACCCCAACCACC

TACTCGTCCCACCGCACAGAACCCGGCGCTATTATGGCAAGAAACTTGAGCAGCCT
601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 660
ATGAGCAAGGGTGGCGTGTCTGGCCGCGGATAATAACCGGTTCTTGAACTCGTCGGA

GTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAGAGACGTG
661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 720
CAAAACTTTCAAGGAGCGAGTCTTACGGTCAACGTCTACCGATTAGTTCTCTGCAC

Fig. 8

2nd half of the
2.p53-BE
 (promoter)

AGCTTTTGGCTACATTTTTATTGTAAAG
 448 -----+-----+-----+-----+ 480
 TCGAAAAACCGATGTAAAAAAATAAACATTTC

TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC
 481 -----+-----+-----+-----+-----+-----+ 540
 ATTCAAATTATTAGTAGTGAGTAGTGACCCGATATTACTATTCATAATTCAATTCTCTAG

CACATATGTGAGTTGCTGGCTTATAATTCAACTCAAGAGATACTGATTGTCAATTGT
 541 -----+-----+-----+-----+-----+-----+ 600
 GTGTATACTCAACGACCGAATATTAAGTGAGTTCTCTATGACTAAAACAGTTAAC

CCTTCCCCCTTTCTCTTCCCTCCATTCCCTTACCTCTCCTTC
 601 -----+-----+-----+-----+-----+-----+ 660
 GGAAAGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGAAATGGAGAGGAAG

CTTCCCTCACACCCCTTCTTCCCTTACATTTTTATTAAATGAACCTTC
 661 -----+-----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGTAAAAAAATAATTACTTGAAAAG

ATTTGGAATAGTTTAGGATTCAAAAATTGCAGAGATAATACAGAGAAATGCCATA
 721 -----+-----+-----+-----+-----+-----+ 780
 TAAAACCTTATCAAATCCTAAAGTTTAAACGTCTATTATGTCTTACGGGTAT

TACCATCCTCTTATCCACTTCTTTGTGTCTATTAGATGCTCAGAGTGTGCACAA
 781 -----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATAGGGTGAAGAAAACACAGATAATCTACGAGTCTCACACACGTGTT

GGCTGGCACGCCAGGGCTTCCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 841 -----+-----+-----+-----+-----+-----+ 900
 CCGACCGTGGGGTCCCAGAAGGAGTACCGTGATTGTCAGATGACTTCCACCTTGTCTC

ACAAGCCTATCAACACCTACAAGACTGGTGTAAAGTGCAGTGACAGATGCAAACACAGG
 901 -----+-----+-----+-----+-----+-----+ 960
 TGTTCGGATAGTTGTGGATGTTCTGACCACATTACGTCACTGTCTACGTTGTGTC

GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA
 991 -----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTCGGGAGTCCTCCATTGGATGGATCTAAACTCCGGGTTGTCCGAGGT

GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 CTTCTTTACAGTTGACTCTCCTCGGACTCCTACTGTCAACCGATTGTTCCCAAT

Fig. 8 (cont'd I)

←--- 3.p53-BE ---→
(promoter)

1081	TTAATGTGTTATTAAATGGGTTGAATCTAATTGGGAAGGGAGAGAGGTTCAGAGTGAGGT AATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAAACGTCTCACTCCA	1140
1141	GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTAGTGTGTCAGTCAGGAA CGTCTCGAACCCACCTGCTACGGTTCCCTATGACTTGGAAATCACACAGGTAGACCTT	1200
1201	CTGCATCCAATTCAAGGTTCAGTAATGATGTCATTATCCAACACATACCTCTGTAAAATT GACGTAGGTTAAGTCCAAGTCATTACAGTAATAGGTTGTATGGAAGACATTTAA	1260
1261	CATGCTAAACTACCTAACGAGCTATCACCCTCCAAAGCAATAGTGACTTGAACAGTGT GTACGATTGATGGATTCTCGATAGATGGCAAGGTTCGTTATCACTGAAACTTGTACAA	1320
1321	TCACCAAGGACAGGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAATAAT AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAA	1380
1381	GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCCATTG CTCATTGCTTCTGCTTCACTAACACTACAAATTATATCGACCCCCATACTGCTAAC	1440
1441	GCTTAAGTTAGCTTGTGTTCTCTTGAGAAAATAAAACTAAGGGCCCTCCCTTT CGAATTCAACAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCCGGGAGGGAAAA	1500
1501	CAGAGCCCTATGGCGAACATCTGACTTTCATATGGTAACGTCCATTCCAGGAAC GTCTCGGGATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGGTCTTG	1560
1561	GTCTGTGAGCCTCTCATGTTGAGCCACAAACATGGACAGCCCAGTCAAATGCCCGCAAG CAGACACTCGGAGAGTACAACGTCGGTGTGACCTGTCGGTCAGTTACGGGGCGTTC	1620
1621	TCTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGC AGAAAGAGACTCACTGAGGTGTTAACCGGTTCCGAGGACATGGTCCGTGGAGACG	1680
1681	GCTCTGAGCTCCATTCTCTTCAAGACCTCCCCAACTTCCCAGGTTGAACTACAGCAGAA CGAGACTCGAGGTAAAGAGGAAGTTCTGGAGGGTTGAAGGGTCAAACTTGATGTCGTCTT	1740
1741	GCCTTAGAAAGGGCAGGAGGCCGGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC CGGAAATCTTCCGTCTCCGGCCAGAGCTCCAGGAGTGGACTTCACTCGTACGGTCTG	1800
1801	CACTGCAGGAACGCCCGGGACAGGAATGCCATTGTCAGAAGCAGAACCTGACTCCTTCC GTGACGTCTTGCGGGGCCCTGTCCTTACGGGTAAACACGTTGCTGGACTGAGGAAGG	1860
1861	TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCGCAGGCCAAGTTGCTGAATCAATGGAGC AGTGGGACTGAAGAGGGGAGGGATGGCGCGTCCGGITCAACGACTTAGTTACCTCG	1920

Fig. 8 (cont'd II)

CCTCCCCAACCGGGCGTCCCCAGCGAGGCTTCTTCCCATCCTCCGTACCACCGGGGC
 1921 -----+-----+-----+-----+-----+-----+ 1980
 GGAGGGGTTGGGCCCGCAAGGGTCGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

TTTCGTGAGCTCGTCTCTGATCTCGCGCAAGAGTGACACACAGGTGTCAAAGACGCTT
 1981 -----+-----+-----+-----+-----+-----+ 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCCTCTCACTGTGTGTCACAAGTTCTGCGAA

CTGGGGAGTGAGGGAAAGCGGTTACCGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG
 2041 -----+-----+-----+-----+-----+-----+ 2100
 GACCCCTCACTCCCTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCCCGTGAC

GCACCGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGGCGAGCTGCCTTTCTCCCGC
 2101 -----+-----+-----+-----+-----+-----+ 2160
 CGTGCCTTGTGTGGACTCCGGTCGGGACCGACGGGTCCGCCTCGACGGAGAAGAGGGCG

GCACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCCGTGACCTTAAGCTTA
 2161 -----+-----+-----+-----+-----+-----+ 2220
 CCTGTACATGTCTCGAGCTCTCATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

←---4.p53-BE---
(intron)

GGGTGGCTGGAGGGGACCCGGTTGGAGAGAGGGAGCGGAACCTGGACAGCCCTGAC
 2221 -----+-----+-----+-----+-----+-----+ 2280
 CCCAGCGACCTCCCCCTGGGGCCAACCTCTCTCGCCTTGAGGACCTGTTGGACTG

----→

AAGCCAAGCAAAGGTCCGCTCCGGCGGGTGGGTGAGTGCAGGCCGCCGGCGGGGC
 2281 -----+-----+-----+-----+-----+-----+ 2340
 TTCCGGTTGGTTCCAGGCCAGGCCGCCACCCACTCAGCGCGGCCGGCGCCCCCG

GGGGAGAGAGCCTGCAGCCTTCAGAACAGATATTGCTCATTTCTGGCAGTTCTCAGACG
 2341 -----+-----+-----+-----+-----+-----+ 2400
 CCCCTCTCTCGGACGTGGAAAGTCTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC

TAGGAAATAAGTCAGCACCGAACGAGTGGTAAGCCGGAGGGCTCGGAAGAACGGCACCT
 2401 -----+-----+-----+-----+-----+-----+ 2460
 ATCCCTTATTCAAGTCGTGGCTCGTCACCAATTGGCCTCCGAGCCTTGTGCCGTGGA

TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTTCTGGAGGCTTACCGTT
 2461 -----+-----+-----+-----+-----+-----+ 2520
 AAAGAAAAGAGCTTTCAATATACCCCCGACTTACTCGAACGACCTCCGAACAAATGGCAA

TTTATTGTACACAGAAAAGGAAACTGCCTTGTCTCCCTCCGGAAATTCTCTCTTAA
 2521 -----+-----+-----+-----+-----+-----+ 2580
 AAAATAACAGTGTGTCTTCCTTGACGGAACAGAGGGAGGCCCTTAAGAGAGAAATT

GACTGTAAGTCGCTGCCCTGAGTGGTTCTGGTCTTCTGGCTTCTCTCTTCT
 2581 -----+-----+-----+-----+-----+-----+ 2640
 CTGACATTCAAGCGACGGACTCACCAAGTAAACAAAACAAAAGACGGGAAGAGAAAGA

TCTTTGCCCTTCTTAGCTGCACTCCCATGGTGAATTCTGCTGGTCTCTGCTGGGG
 2641 -----+-----+-----+-----+-----+-----+ 2700
 AGAAAACGGGAAAGAACGTGAGGGTACCAACTAAAGACGAACCAGAGGACGACCCC

11/26

Fig. 8 (cont'd III)

TTGGTGGTACTCGTCCCCACCGCACAGAACCCGGCGCTATTATTGGCCAAGAAACTTGA
2701 -----+-----+-----+-----+-----+-----+-----+ 2760
AACCACCATGAGCAAGGGTGGCGTCTGGGCCGCGATAATAACCGGTTCTTGAACT

GCAGCCTGTTTGAAAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAATCAAAG
2761 -----+-----+-----+-----+-----+-----+-----+ 2820
CGTCGGACAAACTTTCAAGGGAGCGAGTCTTACGGTCGAACGTCTACCGATTAGTTTC

AGACGTG
2821 ----- 2827
TCTGCAC

12/26

Fig. 9

<---- 1.p53-BE --

TGAGGACTCTAGGAATATGCTGGTAAAATAACCTTAGAGATGCCAACTGT
1 -----+-----+-----+-----+-----+-----+ 60
ACTCCTGAGAGTCCTATACGACCATTATTTATTGAAATCTACGGGTTGACA

-->

TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATTCAATAGATTCTCAAAGGATTCCA
61 -----+-----+-----+-----+-----+-----+ 120
AAAGGGGTCTGTGGTCGTAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCTAAGGT

AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCAACCCTTGACATTAGCATA
121 -----+-----+-----+-----+-----+-----+ 180
TTCCGTTCTCAAACCCCTGTATATATAATTAAATGGGTTGGGAAACTGTAATCGTATG

TAAGGGCCCTGAGAAGTTGGATTAAGAAAGTTCAAATTAAAGTAACCCAGAATT
181 -----+-----+-----+-----+-----+-----+ 240
ATTCCCAGGACTCTCAAAACCTAATTCTTCAAAGTTAATTCAATTGGGCTTAAAA

CTAAGATTATTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCTATCTCCT
241 -----+-----+-----+-----+-----+-----+ 300
GATTCTAATAAACTGGTACTTTGTATACAGAGGGGTGTTCGTGATAAGGATAGAGGAA

GAACTTGAGGATAATTAGACGTACGTGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA
301 -----+-----+-----+-----+-----+-----+ 360
CTTGAACTCCTATTAACTGCATGCACCCATCTCCATCCCCATCCCCATACCGTATCT

AAGAGCAGGACCTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTAA
361 -----+-----+-----+-----+-----+-----+ 420
TTCTCGTCCTGGAACCCCTCGTTATAGATTCAAATTAAAGGACTGAGACGATAATAAT

<---- 2.p53-BE ---->

ACTAACCATTTGCCATGTTGCTTAAGCTTTGGCTACATTTTTATTGTAAAG
421 -----+-----+-----+-----+-----+-----+ 480
TGATTGGTAGAAACGGTACAACGAATTCAACGAAAAACCGATGAAAAAAATAACATT

TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAAGTAAGGAAGATC
481 -----+-----+-----+-----+-----+-----+ 540
ATTCAAATTATTAGTGAGTAGAGTGACCGATATTACTATTCAATTCAATTCTCTAG

CACATATGTGAGTTGCTGGCTATAATTCAACTCAAGAGATACTGATTTGTCAATTGT
541 -----+-----+-----+-----+-----+-----+ 600
GTGTATACACTCAACGACCGAATTAAAGTGTGAGTTCTCTATGACTAAAACAGTTAAC

CCTTCCCCCTTTCTCTTCCCTCCTCATTCCCTTACCTCTCCCTTC
601 -----+-----+-----+-----+-----+-----+ 660
GGAAAGGGAAAAAGAGAGAAGGGAGGAAGGTAAAGGAAGGAATGGAGAGGAAG

Fig. 9 (cont'd !)

CTTCCCTCACACCCCTTCCTTACATTTTATTAAATGAACCTTC
 661 -----+-----+-----+-----+-----+-----+ 720
 GAAGGGAGTGTGGGAAAAGGAAGGAAGAAAATGAAAAAATAATTACTGAAAAG

 ATTTGGAATAGTTTAGGATTCAAAAATTGCAGAGATAATACAGAGAATGCCATA
 721 -----+-----+-----+-----+-----+-----+ 780
 TAAACCTTATCAAATCTAAAGTTTAAACGTCTATTATGTCCTACGGGTAT

 TACCATCCTCTTATCCCACCTCTTTGTGTCTATTAGATGCTCAGAGTGTGCACAA
 781 -----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATAGGGTAAGAAAAACAGATAATCTACGAGTCTCACACACGTGTT

 GGCTGGCACGCCAGGGCTTCCTCATGGCACTAACAGTCACTGAAAGGTGGAACAGAG
 841 -----+-----+-----+-----+-----+-----+ 900
 CCGACCGTGCGGGTCCCAGAAGGAGTACCGTATTGTCAGATGACTTCCACCTGTCTC

 ACAAGCCTATCAACACCTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 901 -----+-----+-----+-----+-----+-----+ 960
 TGTCGGATAGTGTGGATGTTCTGACCACCATTACGTCACTGTCAGTGTGTTGTGTC

 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAAACAGGCTCCA
 991 -----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTCGGGAGTCCTCCATTGGATTGATCTAAACTCCGGTTGTCCGAGGT

 GAAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 CTTCTTTACAGTTGACTCTCCTCGGACTTCCTACTTGTCAACCGATTGTTCCAAAT

 TTAATGTGTTATTAATGGGTGAATCTAATTGGAAGGGAGAGAGGTTGCAGAGTGAGGT
 1081 -----+-----+-----+-----+-----+-----+ 1140
 AATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCA

 GCAGAGCTTGGTGGACGATGCCAAAGGAATACTGAAACCTTAGTGTGTCAGTCTGGAA
 1141 -----+-----+-----+-----+-----+-----+ 1200
 CGTCTCGAACCCACCTGCTACGGTTCCATTGACTTGGAAATCACACAGGTGACACCTT

 CTGCATCCAAATTCAAGGTTCACTGATTGATGTCATTATCCAAACATACCTCTGTAAAATT
 1201 -----+-----+-----+-----+-----+-----+ 1260
 GACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTAA

<---- 3.p53-BE ---->

CATGCTAAACTACCTAACAGAGCTATCTACCGTTCAAAGCAATAGTGACTTGAACAGTGT
 1261 -----+-----+-----+-----+-----+-----+ 1320
 GTACGATTGATGGATTCTCGATAGATGGCAAGGTTCGTTACTGAAACTTGTCA

 TCACCAAGAGCACGAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAAATAAT
 1321 -----+-----+-----+-----+-----+-----+ 1380
 AGTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAA

 GAGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTG
 1381 -----+-----+-----+-----+-----+-----+ 1440
 CTCATTGCTCCTGTCCTCATTAACACTTACAAATTATCGACCCGATACGCTAAAC

 GCTTAAGTTGTTAGCTTCTTCTTGAGAAATAAAAACATAAGGGGCCCTCCCTTT
 1441 -----+-----+-----+-----+-----+-----+ 1500
 CGAATTCAACAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCCGGAGGGAAAA

 CAGAGCCCTATGGCGAACATCTGACTTTCATATGGTAACGTGTCATTCCAGGAAC
 1501 -----+-----+-----+-----+-----+-----+ 1560
 GTCTCGGGATACCGCGTTGAGACATGAAAAGTATACCAATTGACAGGTAAAGTCCTG

Fig. 9 (cont'd II)

1561 GTCGTGAGCCCTCATGTTGCAGCCACAACATGGACAGCCCAGTCAAATGCCCGCAAG + 1620
 CAGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGTCAGTTACGGGGGTTC

 1621 TCTTCTCTGAGTGACTCCAGCAATTAGCCAAGGCTCCTGTACCCAGGCAGGACCTCTGC + 1680
 AGAAAGAGAGACTCACTGAGGTGTTAATCGGTCAGGACATGGTCCGTCTGGAGACG

 1681 GCTCTGAGCTCCATTCTCCTCAAGACCTCCCCAACTTCCAGGTTGAACACAGCAGAA + 1740
 CGAGACTCGAGGTAAGAGGAAGTTCTGGAGGGTTGAAGGGTCAAACTTGATGTCGTCTT

 1741 GCCTTAGAAAAGGGCAGGAGGCCGGCTCTGAGGTCTCACCTGAAGTGAGCATGCCAGC + 1800
 CGGAAATCTTCCCCTCCGGCCAGAGCTCCAGGAGTGGACTTCACGTACGGTCG

 1801 CACTGCAGGAACGCCCCGGGACAGGAATGCCATTGTGCAACGAACCCGTACTCCTCC + 1860
 GTGACGTCTTGCGGGGCCCTGTCCTACGGTAAACACGTTGCTTGGACTGAGGAAGG

 1861 TCACCCCTGACTTCTCCCCCTCCCTACCCGCGCAGGCCAAGTTGCTGAATCAATGGAGC + 1920
 AGTGGGACTGAAGAGGGGGAGGGATGGCGCGCGTCCGGTCAACGACTTAGTTACCTCG

 1921 CCTCCCCAACCGGGCGTCCCCAGCGAGGCTCCTCCATCCTGACCACCGGGC + 1980
 GGAGGGGTTGGGCCCGCAAGGGGTGCTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCG

 1981 TTTCGTGAGCTCGTCTGATCTCGCGCAAGAGTGACACACAGGTGTTCAAAGACGCTT + 2040
 AAAAGCACTCGAGCAGAGACTAGAGCGCGTTCTCACTGTGTGTCACAAGTTCTGCGAA

 2041 CTGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGCGGGCACTG + 2100
 GACCCCTCACTCCCTCGCCAAATGCTCACTGAACCGACCTCGGAGTCCCCGCCGTGAC

 2101 GCACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCCAGCTGCCCTTCTCCGC + 2160
 CGTGCCTTGTGTGGACTCCGGTCGGACCGACGGTCCGCCCTGACGGAGAACAGGGCG

 2161 GGACATGTACAGAGCTCGAGAAGTACTAGTGGCACGTGGCGTGCACCTTAAGCTTA + 2220
 CCTGTACATGTCTCGAGCTTCAATGATCACCGGTGCACCCGGCACGTGGAATTGAAAT

<---- 4.p53-BE
(intron) ---->

2221 GGGTCGCTGGAGGGGACCCCGGTTGGAGAGAGGAGCGGAACCTCTGGACAAAGCCCTGAC + 2280
 CCCAGCGACCTCCCCCTGGGCCAACCTCTCTCCTCGCCTGAGGACCTGTTGGGACTG

----->

2281 AAGCCAAGCCAAAGGTCCGCTCCGGCGGGTGGTGAGTGCGCGCCGCCCGCGGGGCG + 2340
 TTCCGGTTCGGTTCCAGGCGAGGCCGCCACCCACTCACGCGCGCCGGGCGCCCG

2341 GGGGAGAGAGCCTGCAGCCTTCAGAACAGATAATTGCTCATTTCTGGCAGTTCTCAGACG + 2400
 CCCCTCTCTCGGACGTGGAAAGTCTGTCTATAACGAGTAAAGACCGTCAAGAGTCTGC

Fig. 9 (cont'd III)

TAGGAAATAAGTCAGCACCGAACAGCAGTGGTTAAGCCGGAGGGCTCGGAAGAACGGCACCT
 2401 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2460
 ATCCCTTATTCACTCGTGGCTTCGTACCAATTCCGGCTCCCGAGCCTTGTGCCGTGGA

 TTTCTTCTCGAAAAAGTTATATGGGGCTGAATGAGCTCTGGAGGCTTGTACCGTT
 2461 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2520
 AAAGAAAGAGCTTTCAATATACCCCCGACTTACTCGAACGACCTCCGAACAAATGGCAA

 TTTTATTGTACACAGAAAAGGAAACTGCCTTGCTCCCTCCGGAAATTCTCTTTAA
 2521 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2580
 AAAATAACAGTGTGTCTTTCTTGACGGAACAGAGGGAAAGGCCCTTAAGAGAGAAATT

 GACTGTAAGTCGCTGCCTGAGTGGTTCATTTGTTTCTGCCCTCTCTTTCT
 2581 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2640
 CTGACATTCAAGCGACGGACTCACCAAGTAAAACAAAACAAAAGACGGGAAGAGAAAGA

 TCTTTGCCCTTCTTAGCTTGCACTCCCAGGTGATTCGCTGGTCTCCTGCTGGGG
 2641 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
 AGAAAAACGGGAAAGAACGAAACGTGAGGGTACCACTAAAGACGAACCAAGAGGACACCC

 TTGGTGGTACTCGTCCCACCGCACAGAACCGGCGCTATTATTGCCAAGAAACTTGA
 2701 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2760
 AACCAACATGAGCAAGGGTGGCGTGTCTGGGCCGCGATAATAACCGTTCTTGAAC

 GCAGCCTGTTTGAAGTCCCTCGCTCAGAAATGCCAGCTGCAGATGGCTAACCAAAG
 2761 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 2820
 CGTCGGACAAAACCTTTCAAGGGAGCGAGTCITACGGTCAACGTCTACCGATTAGTTTC

 AGACGTG
 2821 ----- 2827
 TCTGCAC

DRAFT - NOT FOR CITATION

Fig. 10

<---- 1.p53-BE ----
(promoter)

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TGAGGACTCTAGGAATATGCTGGAAAATAACCTTAGAGATGCCAAACTGT
1 -----+-----+-----+-----+-----+-----+-----+ 60
ACTCCTGAGAGTCCTTATACGACCATTATTTTATTGAAATCTCTACGGGTTGACA
-->

TTTCCCCAGAACACCAGCATTCAATTAGGTGTTCAATAGATTCTCAAAGGATTCCA
61 -----+-----+-----+-----+-----+-----+-----+ 120
AAAGGGGTCTTGTGGTCGAAGTAATCCACAAGTAAGTTATCTAAGAAGTTCCCTAAGGT
AAGGCAAAGAAGTTGGGAACAGTATATATAATTACCCAACCCCTTGACATTAGCATA
121 -----+-----+-----+-----+-----+-----+-----+ 180
TTCCGTTCTCAAACCCCTGTCAATATATTAATGGGTGGGAAACTGTAATCGTATG
TAAGGGCCCTGAGAAGTTGGATTAAAGAAAGTTCAAAATTAAAGTAACCCAGAATT
181 -----+-----+-----+-----+-----+-----+-----+ 240
ATTCCCAGGACTCTCAAACCTAATTCTTCAAAGTTAATTCAATTGGGTCTAAAA
CTAAGATTATTGACCATGAAACATATGTCCTCCCACAAAGCACATATTCCATCTCCTT
241 -----+-----+-----+-----+-----+-----+-----+ 300
GATTCTAATAAACTGGTACTTGTATACAGAGGGGTGTTCGTGTATAAGGATAGAGGAA
GAACCTGAGGATAATTAGACGTACGTGGGTAGAGGGTAGGGGAAGGGGTATGGCATAGA
301 -----+-----+-----+-----+-----+-----+-----+ 360
CTTGAACCTCTATTAATCTGCATGCACCCATCTCCATCCCCTCCCCATACCGTATCT
AAGAGCAGGACCTGGGAGCAAGAATATCTAAGTTAATTCTGACTCTGCTATTATTA
361 -----+-----+-----+-----+-----+-----+-----+ 420
TTCTCGTCTGGAACCCCTCGTTCTATAGATTCAAATTAGACTGAGACGATAATAAT

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<---- 2.p53-BE ---->
(promoter)

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ACTAACCATTTGCCAATGTTGCTTAAGCTTTGGCTACATTTTTATTGTAAAG
421 -----+-----+-----+-----+-----+-----+-----+ 480
TGATTGGTAGAAACGGTTACAACGAATTGAAAAACCGATGTAAAAAAAACATTTC
TAAGTTAATAATCACTCATCTCACTGGCTATAATGATAAGTATTAAGTAAGGAAGATC
481 -----+-----+-----+-----+-----+-----+-----+ 540
ATTCAAATTATTAGTGAGTAGAGTGACCCGATATTACTATTCTAATTCTTCTAG
CACATATGTGAGTTGCTGGCTATAATTCAACACTCAAGAGATACTGATTTGTCATTGT
541 -----+-----+-----+-----+-----+-----+-----+ 600
GTGTATACACTCAACGACCGAATATTAAGTGTGAGTTCTATGACTAAAACAGTTAAC
CCTTCCCCTTTTCTCTCTTCCCTCCATTCTTACCTCTCCCTTC
601 -----+-----+-----+-----+-----+-----+-----+ 660
GGAAAGGGGAAAAAAAGAGAGAAGGGAGGAAGGTAAGGAAGAAGGGATGGAGAGGAAAG
CTTCCCTCACACCCCTTCCCTTACATTTTATTAAATGAACTTTCT
661 -----+-----+-----+-----+-----+-----+-----+ 720
GAAGGGAGTGTGGGAAAGGAAGGAAGAAAATGTAaaaaAAATTTACTTGAAAAG
ATTGGAAATAGTTAGGATTCAAAATTCAGAGATAATACAGAGAATGCCATA
721 -----+-----+-----+-----+-----+-----+-----+ 780
TAAACCTTATCATAACCTAAAGTTAAACGTCTATTATGCTCTACGGGTAT

```

Fig. 10 (cont'd I)

TACCATCCTCCTTATCCCACTTCTTTGTCTATTAGATGCTCAGAGTGTGCACAA
 781 -----+-----+-----+-----+-----+-----+-----+-----+ 840
 ATGGTAGGAGGAATAGGGTGAAGAAAAACACAGATAATCTACGAGTCTCACACACGTGTT

 GGCTGGCACGCCAGGGTCTCCTCATGGCACTAACAGTCTACTGAAAGGTGGAACAGAG
 841 -----+-----+-----+-----+-----+-----+-----+-----+ 900
 CCGACCCTGCGGGTCCCAGAAGGAGTACCGTGATTGTCAAGATGACTTCCACACTGTCTC

 ACAAGCCTATCAACACACTACAAGACTGGTGGTAAGTGCAGTGACAGATGCAAAACACAGG
 901 -----+-----+-----+-----+-----+-----+-----+-----+ 960
 TGTCGGATAGTTGTGGATGTTCTGACCACCATCACGTCACTGTCACTGTTGTGTC

 GTGATGGAAAGCCCTCAGGAGGGTAACCTAACCTAGATTGAGGGCCAACAGGCTCAG
 961 -----+-----+-----+-----+-----+-----+-----+-----+ 1020
 CACTACCTTCGGGAGTCCTCCATTGGATTGGATCTAAACTCCGGTTGTCCGAGGTC

 AAGAAAATGTCAACTGAGAGGAAGCCTGAAGGATGAACAGTGGCTAAGCAAAGGGTTAT
 1021 -----+-----+-----+-----+-----+-----+-----+-----+ 1080
 TTCTTTACAGTTGACTCTCCTCGGACTTCACTTGTCAACCGATTCGTTCCAATA

 TAATGTGTTATAATGGGTGAATCTAATTGGGAAGGGAGAGAGGTTGCAGAGTGAGGTG
 1081 -----+-----+-----+-----+-----+-----+-----+-----+ 1140
 ATTACACAATAATTACCCAACCTAGATTAACCCCTCCCTCTCCAACGTCTCACTCCAC

 CAGAGCTTGGTGGACGATGCCAAGGAATACTGAAACCTTCTAGTGTGTCAGTCAGGAAAC
 1141 -----+-----+-----+-----+-----+-----+-----+-----+ 1200
 GTCTCGAACCACTGCTACGGTTCTTATGACTTGGAAATCACACAGGTCAAGACCTTG

 TGCACTCAAATTCAAGGTTAGTAATGATGTCATTATCAAACATACCTTCTGTAAAATT
 1201 -----+-----+-----+-----+-----+-----+-----+-----+ 1260
 ACGTAGGTTAAGTCCAAGTCATTACTACAGTAATAGGTTGTATGGAAGACATTTAAG

<---- 3.p53-BE ---->

(promoter)

ATGCTAAACTACCTAAGAGCTATCTACCGTTCAAAGCAATAGTGACTIONGAACAGTGT
 1261 -----+-----+-----+-----+-----+-----+-----+-----+ 1320
 TACGATTGATGGATTCTCGATAGATGGCAAGGTTCTGTTATCACTGAAACTTGTCAAA

 CACCAAGCAGCAAAGAATTACAAGATTTTTAAAGAAAATTGCCAGGAATAATG
 1321 -----+-----+-----+-----+-----+-----+-----+-----+ 1380
 GTGGTCTCGTCTTCTTAATGTTCTAAAAAAATTCTTTAACCGGTCTTATTAC

 AGTAACGAAGGACAGGAAGTAATTGTGAATGTTAATATAGCTGGGCTATGCGATTGG
 1381 -----+-----+-----+-----+-----+-----+-----+-----+ 1440
 TCATTGCTTCTGTCTTCATTAACACTACAAATTATATCGACCCCCGATACGCTAAACC

 CTTAAGTTGTTAGCTTGTCTCTTGAGAAAATAAAACTAAGGGCCCTCCCTTTC
 1441 -----+-----+-----+-----+-----+-----+-----+-----+ 1500
 GAATTCAACAAATCGAAACAAAAGGAGAACTCTTATTTGATTCCCGGGAGGGAAAAG

 AGAGCCTATGGCGAACATCTGTACTTTCTATATGGTTAATGTCCATTCCAGAAACG
 1501 -----+-----+-----+-----+-----+-----+-----+-----+ 1560
 TCTCGGAATACCGCGTTGAGACATGAAAAAGTATACCAATTGACAGGTAAAGGTCTTGC

 TCTGTGAGCCTCTCATGTTGAGCCACAAACATGGACAGGCCAGTCAGTAAATGCCCGCAAGT
 1561 -----+-----+-----+-----+-----+-----+-----+-----+ 1620
 AGACACTCGGAGAGTACAACGTCGGTGTACCTGTCGGGTCACTTACGGGGCGTTCA

 CTTCTCTGAGTGACTIONCCAGCAATTAGCCAAGGCTCTGTACCCAGGCAGGACCTCTGCG
 1621 -----+-----+-----+-----+-----+-----+-----+-----+ 1680
 GAAAGAGACTCACTGAGGTCGTTAATCGGTTCCGAGGACATGGTCGTCCCTGGAGACGC

 CTCTGAGCTCATTCTCCTCAAGACCTCCCCACTTCCAGGTTGAACATACAGCAGAAG
 1681 -----+-----+-----+-----+-----+-----+-----+-----+ 1740
 GAGACTCGAGGTAAGAGGAAGTTCTGGAGGGGTGAAGGGTCCAACITGATGTCGTCTTC

Fig. 10 (cont'd II)

1741 CCTTTAGAAAGGGCAGGAGGCCGCTCTCGAGGTCCACCTGAAGTGAGCATGCCAGCC
 GGAAATCTTCCCCGTCCCTCCGGCGAGAGCTCCAGGAGTGGACTTCACGTACGGTCGG
 1801 ACTGCAGGAACGCCCGGGACAGGAATGCCATTGTGCAACGAACCCCTGACTCCTCCT
 TGACGTCCCTGCGGGGCCCTGTCCCTACGGTAAACACGTTGCTTGGACTGAGGAAGGA
 1861 CACCCCTGACTTCTCCCCCTCCCTACCCGCGCGAGGCCAAGTTGCTGAATCAATGGAGCC
 GTGGGACTGAAGAGGGGAGGGATGGCGCGTCCGGTTCAACGACTTAGTTACCTCGG
 1921 CTCCCCAACCGGGCGTCCCCAGCGAGGCTTCTTCCCACCTCCTGACCACCGGGGCT
 GAGGGGTTGGGCCCGCAAGGGTGTCCGAAGGAAGGGTAGGAGGACTGGTGGCCCCGA
 1981 TTTCGTGAGCTCGTCTGATCTCGCGCAAGAGTGACACACAGGTGTTAAAGACGCTTC
 AAAGCACTCGAGCAGAGACTAGAGCGCGTCTCACTGTGTGTCACAAGTTCTGCGAAG
 2041 TGGGGAGTGAGGGAAAGCGGTTACGAGTGACTTGGCTGGAGCCTCAGGGGCGGGACTGG
 ACCCCTCACTCCCTCGCCAATGCTCACTGAACCGACCTCGGAGTCCCCGCCGTGACC
 2101 CACGGAACACACCCCTGAGGCCAGCCCTGGCTGCCAGGCGGAGCTGCCCTTCTCCCCGG
 GTGCCTTGTGTGGACTCCGGTCGGACCGACGGTCCGCTCGACGGAGAACAGGGCGC
 2161 GTTGGTGGACCCGCTCAGTACGGAGTTGGGAAGCTTTCACTTCGGAGGATTGCTCA
 CCAACCACCTGGCGAGTCATGCCCTAACCCCTCGAGAAAGTGAAGCCTCTAACGAGT
 2221 ACAACCATGCTGGGCATCTGGACCCCTCACCTCTGGTGATCCCTCTCCTGCCCGGGTGG
 TGTTGGTACGACCCGTAGACCTGGAGGATGGAGACCCTAGGGAGAGGACGGGCCACC
 2281 AGGCTTACCCGTCTAGTCCGGGGATAGGCAAAGTGGGGCGCGGGACGCGTGG
 TCCGAATGGGGCAGAATCAGGGCCCTATCCGTTACCCCGCCCGCCCTGCGCACGC
 2341 GGATTGCAGGGCAGCGCGCACGCCGACCTGGAGCGGGCTGCTGCCGGAGGCG
 CCTAACGCGCCGTGGCGCGTGGACCCCTGCCGCCGACGCCCTCCGC
 TTGGAGACTGGCTCCGGGGCTGTTAGGACCTCCCTCAGGCCGGTGCTCAGAACGA
 AACCTCTGACCGAGGGCCCCGACAATCCTGGAAGGGAGTCCGGGCCACGAGTCTTGCT
 2401 TGGAGACTTGCTTTCTTGGGGCTTGATGCGAAGTGCTGATCCGCTGGCAGGCGGG
 AACCTCCTGAACGAAAAGAACCGGAACCTACGCTTCACGACTAGGGGAGCCGACCCGTCCGCC
 2461 CAGCTCCGGCGCTCCCGGAGACCAACTGCGCTCCACGTTGAGGTGGCGTGGGGCGGA
 GTCGAGGCCGAGGAGCCTGGTGACGCCAGGTGCAACTCCACCCGCACCCCCCGCCT
 2521 CAGGAATTGAAGCGGAAGTCTGGGAAGCTTGGGTGCGTGGAGGGGACCCCGGTTGGA
 GTCCCTTAACCTCGCCTTCAGACCCCTCGAAATCCAGCGACCTCCCCCTGGGCCAACT
 2581

<---- 4.p53-BE ---->

(intron)

2641 GAGAGGAGCGGAACCTCTGGACAAGCCCTGACAAGCCAAGGCCAAAGGTCCGCTCCGGCGC
-----+-----+-----+-----+-----+-----+-----+-----+-----+ 2700
CTCTCCTCGCCTTGAGGACCTGTTGGACTGTTGGTTCGGTTCCAGGCAGGCCGCG

Fig. 10 (cont'd III)

2701	GGGTGGGTGAGTGC CGCCGCCCGCGGGGGAGAGAGCCTACAGC TT CAGAACA CCCACCCACTCAC GCGCGGCGGGCGCCCCCGCCCTCTCGGATGTC GGAAGTCTTGT	2760
2761	CATATTGCTCATTTCTGGCAGTTCTCAGACGTAGGAAATAAGTCAGCACCGAACAGTG GTATAACGAGTAAAAGACCGTCAAGAGTCTGCATCCTTATTCAAGTCGTGGCTTCGTCAC	2820
2821	GTAAAGCCGGAGGGCTCGGAAGAACGGCACCTTCTCGAAAAAGTTATATGGGGG CAATT CGGCCTCCCGAGCCTTCTGCCGTGGAAAAGAAAGAGCTTTCAATATAACCCC	2880
2881	CTGAATGAGCTCTGGAGGCTTACCGTTTTTATTGTCACACAGAAAAGGAAACTG GACTTACTCGAAGACCTCCGAACAAATGGCAAAAATAACAGTGTCTTTCCCTTGAC	2940
2941	CCTTGTCTCCCTTCCGGAAATTCTCTCTTAAGACTGTAAGTCGCTGCCTGAGTGGTTTC GGAACAGAGGGAGGCCCTTAAGAGAGAAATTCTGACATT CAGCGACGGACTCACCAAAG	3000
3001	ATTTTGT TTTGTTTCTGCCCTCTCTTTCTCTTTGCCCTTCTTAGCTTGC ACTCC TAAAACAAAACAAAAGACGGGAAGAGAAAGAAGAAAAGGGAAAGAATCGAACGTGAGG	3060
3061	CATGGTGATTCTGCTTGGTCTCCTGCTGGGGTTGGTGGTACTCGTCCCACCGCACAGA GTACC ACTAAAGACGAACCAGAGGACGACCCCAACCACCATGAGCAAGGGTGGCGTGTCT	3120
3121	ACCCGGCGCCTATTATTGGCCAAGAAACTTGAGCAGCCTGTTGAAAAGTCCCTCGCTC TGGGCCGCGATAATAACCGGTCTTGAACTCGTCGGACAAAACTTTCAAGGGAGCGAG	3180
3181	AGAAATGCCAGCTTGCAGATGGCTAATCAAAG TCTTTACGGTCGAACGTCTACCGATTAGTTTC	3212

Fig 11

variations in the p53 binding region of figure 8

1. p1140 IMI

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMI	GG A AAGCCCTGACAAGCCA
	↑

positions of the mutations (boldface and arrow): 2270 (C→A)

2. p1140 IMII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMII	GG A A AAGCCCTG A A AGCCA
	↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2280 (C→A)

3. p1140 IMIII

p1140	GGACAAGCCCTGACAAGCCA
p1140 IMIII	GG A A A TCCCTG A A ATCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270 (C→A)
2273 (G→T)
2280 (C→A)
2283 (G→T)

4. p1140 IMIV

p1140 GGACAAGCCCTGACAAGCCA
p1140 IMIV **GCACAAGCCCTCACAAGCCA**
 ↑ ↑

positions of the mutations (boldface and arrow): 2268 (G→T)

2278 (C→A)

Fig. 12

variations in the p53 binding regions of figure 9

1. p1141 IMIII

p1141	GGACAAGCCCTGACAAGCCA
p1141 IMIII	GGAA AATCCCTGA AA ATCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2270

2273

2280

2283

2. p1141 1p53

p1141	AGAGATGCCAAACTGTTT
p1141 1p53	AGAGATTCCC AAA AT GTTT
	↑ ↑

positions of the mutations (boldface and arrow): 50

57

3. p1141 2p53

p1141	AATGTTGCTTAAGCTTTTT
p1141 2p53	AATGTT TCTTAAGATTTTT
	↑ ↑

positions of the mutations (boldface and arrow): 443

450

4. p1141 3p53

p1141 AACTACCTAAGAGCTATCT

p1141 3p53 ACAATACCTAAGAGCTATCT

1

positions of the mutations (boldface and arrow): **1268** (A→C)
1270 (C→A)

5. p1141 ΔB_{gl}

<---- 1.p53-BE ---->
p1141 AATAACCTTTAGAGATGCCAACTGTTTCCCCAGAAC
p1141ABg1 AATAACCTTTA-----GATCTCCCCAGAAC

6. p1141 ΔSpe

<---- 2.p53-BE ---->

p1141	CATCTTGGCCAATGTTGCTTAAGCTTTTTGGCTACATT
p1141ABgl	CATCTTGGCCA-----CTAGTGGCTACATT

7. p1141 ΔMph

<---- 3.p53-BE ---->

p1141	AATT CATGCTAAACTACCTAAGAGCTATCTACCGTTCCAA
p1141ABg1	AATT CATGCTATGCA-----TACCGTTCCAA

Fig. 13

varyations in the p53 binding region of figure 10

1. p1142 TAG

mutation of the positions: 2227 (A→T)
 2228 (T→A)

2. p1142 IMIII

p1142	GGACAAAGCCCTGACAAGCCA
p1142 IMIII	GGAAAATCCCTGA AAATCCA
	↑ ↑ ↑ ↑

positions of the mutations (boldface and arrow): 2662 (C→A)
 2665 (G→T)
 2672 (C→A)
 2675 (G→T)

3. . p1142 ΔBgl

<---- 1.p53-BE ---->	
p1142	AATAACCTT TAGAGATGCCAAACTGTTTTCCCCAGAAC A
p1142ΔBgl	AATAACCTT A-----GATCTCCCCAGAAC A

4. p1142 ΔSpe

<---- 2.p53-BE ---->	
p1142	CATCTTGCC AATGTTGCTTAAGCTTTTTGGCTACATT T
p1142ΔBgl	CATCTTGCC A-----CTAGTGGCTACATT T

5. p114² ΔMph

<---- 3.p53-BE ---->

p1142	AATT CATGCTAAACTACCTAAGAGCTATCTACCGTTCAA
p1142ΔBgl	AATT CATGCTATGCA-----TACCGTTCAA

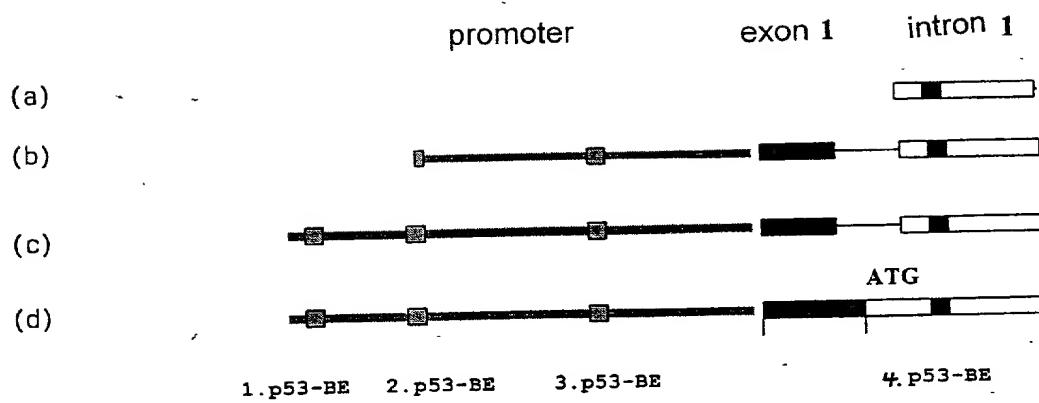


Fig. 14